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GENETIC DIVERGENCE STUDY IN GLADIOLUS

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ABSTRACT

Studies were carried out to find out the most diverse clusters (group of genotypes having similar characteristic features) taking 19 characters for observation among 30 genotypes of gladiolus grown over two successive years in Department of Floriculture and Landscaping. The pooled data was analyzed for divergence study using Mahalanobis's D^2 statistic method. On the basis of D^2 values, the test entries were grouped into 12 clusters following Tocher's method. Thus, it was concluded that inter crossing among genotypes included in diverse clusters is likely to produce potential hybrid which could be maintained and multiplied through asexual reproduction.

KEYWORDS: Genetic Divergence Study in Gladiolus, 19 Characters, 30 Genotypes, Mahalanobis's D^2 Statistic

INTRODUCTION

Gladiolus is considered to be a high value crop next to rose in floriculture trade. The improvement of gladiolus has remained more or less stationary due to lack of good parents. It is a well known fact that choice of parents is of paramount importance in any successful breeding programme. To achieve this prime objective, it is important to understand the genetic divergence for yield and its components in the available germplasm. Selection of parents or lines based on individual attributes may not be advantageous as that based on a number of important components collectively, if the aim is to seek improvement in complex quantitative traits such as yield. Since genetically diverse and geographically isolated lines may generate a wide range variation when brought together, Mahalanobis's D^2 statistic of multivariate analysis serves as an effective tool in the quantitative estimation of genetic diversity both at inter and intra cluster level and a rational choice of potential parents for a breeding programme.

MATERIALS AND METHODS

The present investigation was carried out at Department of Floriculture and Landscaping, College of Agriculture, OUAT, Bhubaneswar for two successive years for divergence study in gladiolus. The experiment consisted of 30 genotypes of gladiolus grown in randomized block design with three replication with a spacing of 30cm x 20cm. Observations were recorded for five plants of each variety under each replication selected randomly taking 19 characters. After testing of differences between genotypes for each of the 19 characters, a simultaneous test of significance of differences in mean values of the 19 correlated variables for 30 genotypes were pooled using Wilk's Lambda (λ) criterion and V-statistics (Rao,1952).

Mahalanobis's (1928) generalized distance, D^2-statistics was used for computing genetic divergence as described by Rao (1952). The original measurements were transformed to standardized uncorrelated variables by pivotal condensation (Rao, 1952). The divergence between any two varieties was obtained as the sum of squares of the difference

in the values of the corresponding transformed values. $D_{ij}^2 = \sum_{i=k} \left(Y_{ij} - Y_{ji}\right)^2$ gives the D^2 between i^{th} and j^{th} varieties for 'k' characters.

The possible pairs of D^2 values were calculated from the 30 genotypes. The statistical significance of each D^2 value was tested by x^2 with p degrees of freedom, p being the number of characters considered for D^2 estimation. The related contribution of individual characters to divergence was assessed by ranking of components of D^2 over all combinations.

Following Tocher's method as described by Rao (1952), the genotypes were grouped into clusters. The criterion of grouping was that any two genotypes belonging to the same cluster should have a smaller D^2 value than those between genotypes belonging to different clusters. Inter and intra-cluster distances were determined and represented.

RESULTS AND DISCUSSIONS

In the present study all the 30 genotypes were grouped on the basis of genetic affinity or diversity as measured by D^2 values which resulted in 12 clusters (Table 1). Cluster-I was the largest having 14 genotypes followed by cluster-II with four, cluster-III with two, cluster-IV with two and cluster-V, VI, VII, VIII, IX, X, XI, XII with one genotype each indicated the genetic proximity of genotypes grouped in one cluster. It is generally suggested that genetic diversity must form the sound base for selecting parents for hybridization rather than ecological diversity (Hazarika *et al.*, 1986). In the past ecological diversity has been largely relied as an index of genetic diversity. This criterion being only inferential, obviously cannot be used for discrimination among population of the same or similar geographical region. It may be more pertinent for so called indigenous or primitive collections which have passed through natural forces of selection, rather than modern varieties. The entries in the present study were mostly improved varieties developed through selection. In consequence of directed artificial selection for early spike emergence, long spikes, long rachis length, length & diameter of floret and more number of florets per spike showing broad similarities were found in the same cluster while those having wider difference were in different clusters. The clustering pattern (Table 1) in the present study indicated that cluster VI had one genotype exhibited earliest emergence of flower spike. Besides, it showed maximum girth, spike diameter and length of florets (Table 1 and 2). On the contrary the single genotype in cluster VII was late flowering type which exhibited maximum delay in emergence of flower spike, showing colour in basal floret as well as opening of basal floret. Genotype in cluster XI exhibited longest spike with longest rachis, highest number of florets and maximum bloom life. Thus, the varieties possessing similar or dissimilar traits for which they had been selected entered into same or different clusters respectively. Similar observation was reported by Bhatt (1970) who suggested that selection could cause greater diversity than eco-geographic distance.

The kind of genetic diversity found among the genotypes belonging to same geographical region might be due to differences in adaptation, selection criteria, selection pressure and environmental conditions (Nayak *et al*., 2004). The genotypes included in the present study showed considerable variation in respect of 19 characters. The relative contribution of different characters to genetic divergence clearly indicated that weight of corm was the major contributing factor followed by number of florets per spike, diameter of corm and rachis length (Table 3). The restricted role of other characters may be attributed to the fact that most of the test entries were commercial varieties.

The classification of genotype through different classificatory analysis like multivariate analysis including D^2 method for quantification of genetic divergence among the set of biological population have been questioned by many authors. There are also instances in D^2 analysis to show that even the different selections from the same cross or from the different crosses can be grouped into same or different clusters respectively depending upon the similarity or dissimilarity of characters.

CONCLUSIONS

The genotypes having varied performance coupled with diversity were grouped into 12 clusters following Tocher's method on the basis of D^2 values for clustering the population into clusters and sub-clusters. Thus this grouping of genotypes has great relevance to the future breeding programme and the genotypes included in diverse clusters are likely to produce potential hybrids. Hybridization of variety Adagio in cluster VIII with White prosperity in Cluster XI is likely to yield F_1 hybrid processing desirable traits. Similarly hybridization of Princess margarate rose in cluster IX with White Prosperity in cluster XI will be beneficial in improvement of gladiolus. Once the desirable hybrids are obtained they could be maintained and multiplied through asexual reproduction for commercial use.

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APPENDICES

Table 1: Distribution of 30 Gladiolus Genotypes in Various Clusters Based on D^2 Analysis

Clusters	Number of Genotypes Included in the Cluster	Name of the Genotypes
I	14	Precillia (V_3), Mascagni (V_4), Bluesky (V_6), Friendship White (V_7), Wingsong (V_8), Plumtart (V_{10}), Novalux (V_{11}), Jester (V_{12}), Traderhorn (V_{16}), Flavosunset (V_{19}), Jessica (V_{20}), Purpleflora (V_{21}), Victorberge (V_{23}), Jacksonville (V_{25})
II	4	Deepset Red (V_{13}), Red-54 (V_{14}), Solist White (V_{26}), Ocillia (V_{27})
III	2	Charisma (V_{18}), NG-35 (V_{24})
IV	2	Chemistry (V_{17}), Huntingsong (V_{29})
V	1	Peterpears (V_2)
VI	1	Grandpics (V_9)
VII	1	Nightmare (V_{28})

Table 1 – Cond.,

VIII	1	Adagio (V_5)
IX	1	Princess margarate rose (V_1)
X	1	Red Beauty (V_{30})
XI	1	White Prosperity (V_{22})
XII	1	Wig's Sensation (V_{15})

Table 2: Cluster Means (D^2 Based) in 30 Gladiolus Genotypes for 19 Characters

Sl. No.	Clusters / Characters	I (14)	II (4)	III (2)	IV (2)	V (1)	VI (1)	VII (1)	VIII (1)	IX (1)	X (1)	XI (1)	XII (1)
1	Plant height(cm)	67.33	69.46	75.30	66.60	71.58	65.78	75.50	**81.28**	**57.80**	69.07	66.95	62.30
2	Girth(cm)	4.31	4.41	4.59	4.49	4.23	**4.93**	4.48	4.37	4.27	4.42	4.73	**4.08**
3	No. of leaves at spike emergence stage	5.85	5.68	5.11	5.32	5.73	5.97	**4.93**	6.03	5.58	**6.47**	5.73	6.07
4	Leaf length(cm)	52.11	52.94	58.90	**46.43**	55.87	49.95	53.97	**62.85**	46.83	57.88	52.90	54.43
5	Leaf width(cm)	2.68	2.70	3.38	2.66	2.97	3.73	2.61	**4.12**	2.93	2.51	**2.47**	3.11
6	Days to emergence of flower spike	57.15	63.72	63.90	57.10	57.07	**55.10**	**73.53**	60.30	58.13	60.47	55.30	67.78
7	Days to show colour of basal floret	64.32	69.98	70.90	63.80	63.82	67.00	**79.40**	67.20	64.40	66.20	**62.13**	75.70
8	Days to opening of basal floret	67.00	72.28	73.10	66.14	**66.53**	67.10	**81.57**	67.67	67.27	68.37	64.43	78.30
9	Length of spike(cm)	65.79	71.10	65.73	58.69	64.83	71.93	66.63	71.23	63.40	**58.63**	**91.17**	66.17
10	Spike diameter(cm)	2.14	2.16	2.19	2.13	2.16	**2.31**	2.17	2.15	2.15	2.15	2.25	**2.12**
11	Rachis length(cm)	48.64	54.45	46.72	39.79	**35.53**	60.73	43.70	54.07	41.47	38.03	**71.12**	46.30
12	No. of florets per spike	10.70	13.47	12.31	11.27	9.90	13.33	10.67	8.77	**5.70**	10.30	**16.33**	10.27
13	Length of floret(cm)	10.90	10.99	10.90	10.36	**8.35**	**12.13**	10.03	10.60	8.73	11.15	10.62	10.65
14	Diameter of floret(cm)	11.70	11.83	11.69	11.01	**9.60**	11.85	10.82	11.32	9.78	**12.07**	11.63	11.40
15	Distance between two florets(cm)	4.31	5.24	4.63	4.11	3.83	4.77	4.92	4.33	**3.53**	4.95	**6.55**	4.13
16	No. of florets remain open at a time	4.09	4.32	**4.98**	4.00	**3.13**	4.93	4.17	4.40	3.53	3.80	4.77	3.43
17	Bloom life of spike	10.59	11.23	11.37	12.37	9.73	12.37	10.57	9.87	**9.37**	10.20	**14.43**	10.37
18	Weight of corm(cm)	18.84	12.13	22.83	20.08	19.67	18.17	16.83	24.00	21.50	**9.17**	12.83	**33.83**
19	Diameter of corm(cm)	4.30	3.19	**4.66**	3.63	4.58	4.17	2.92	4.52	4.32	**2.42**	3.67	3.75

Figures in parentheses indicate number of varieties in a cluster.

Bold figures underlined indicate maximum and bold figures without underline indicate minimum values.

Table 3: Relative Contribution of Different Characters to Genetic Divergence among 30 Gladiolus Genotypes

Sl. No.	Character	Average D^2	% of Total D^2	Rank Total	% of Rank Total
1	Plant height(cm)	8.970	4.93 (9)	3764	4.55 (5)
2	Girth(cm)	2.059	1.13 (16)	5708	6.91 (16)
3	No. of leaves at spike emergence stage	4.912	2.70 (14)	4583	5.54 (12)
4	Leaf length(cm)	6.049	3.33 (12)	4436	5.37 (10)
5	Leaf width(cm)	7.234	3.98 (11)	4405	5.33 (9)
6	Days to emergence of flower spike	8.827	4.85 (10)	3858	4.67 (7)
7	Days to show colour of basal floret	1.367	0.75 (18)	6037	7.30 (17)
8	Days to opening of basal floret	3.064	1.69 (15)	5152	6.23 (14)
9	Length of spike(cm)	10.256	5.64 (6)	4446	5.38 (11)
10	Spike diameter(cm)	0.718	0.39 (19)	6581	7.96 (18)
11	Rachis length(cm)	13.439	7.39 (4)	3501	4.23 (4)
12	No. of florets per spike	25.222	13.87 (2)	2776	3.36 (2)
13	Length of floret(cm)	12.199	6.71 (5)	3835	4.64 (6)
14	Diameter of floret(cm)	1.874	1.03 (17)	5702	6.89 (15)
15	Distance between two florets(cm)	9.502	5.23 (7)	3953	4.78 (8)

Table 3: Contd.,

16	No. of florets remain open at a time	9.413	5.18 (8)	3950	4.78 (8)
17	Bloom life of spike	5.168	2.84 (13)	4614	5.58 (13)
18	Weight of corm(cm)	29.719	16.35 (1)	2561	3.10 (1)
19	Diameter of corm(cm)	21.827	12.00 (3)	2788	3.37 (3)
Total		**181.819**		**82650**	

Figures in parentheses indicate rank (importance).